



1007P1D1seq1 (new)-response to 6-29-04 action.txt  
Patin Docket & Review

## Sequence Listing

### (1) GENERAL INFORMATION:

- (i) APPLICANT: Ashkenazi, Avi J.
- (ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
- (iii) NUMBER OF SEQUENCES: 28
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Genentech, Inc.
  - (B) STREET: 1 DNA Way
  - (C) CITY: South San Francisco
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US/09/993,234A
  - (B) FILING DATE: 19-NOV-2001
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/828683
  - (B) FILING DATE: 31-MAR-1997
- (viii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/625328
  - (B) FILING DATE: 1-Apr-1996
- (ix) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/710802
  - (B) FILING DATE: 23-Sep-1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Marschang, Diane L.
- (B) REGISTRATION NUMBER: 35,600
- (C) REFERENCE/DOCKET NUMBER: P1007P1D1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650/225-5416
- (B) TELEFAX: 650/952-9881

### (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 181 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

Met	Glu	Gln	Arg	Pro	Arg	Gly	Cys	Ala	Ala	Val	Ala	Ala	Leu	
1				5				10					15	
Leu	Leu	Val	Leu	Leu	Gly	Ala	Arg	Ala	Gln	Gly	Gly	Thr	Arg	Ser
				20					25				30	
Pro	Arg	Cys	Asp	Cys	Ala	Gly	Asp	Phe	His	Lys	Lys	Ile	Gly	Leu
				35				40					45	
Phe	Cys	Cys	Arg	Gly	Cys	Pro	Ala	Gly	His	Tyr	Leu	Lys	Ala	Pro
				50					55				60	
Cys	Thr	Glu	Pro	Cys	Gly	Asn	Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln
				65					70				75	
Asp	Thr	Phe	Leu	Ala	Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala
				80				85					90	
Arg	Cys	Gln	Ala	Cys	Asp	Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu
				95					100				105	
Asn	Cys	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly
				110				115					120	
Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	Gln	Cys	Val	Ser	Ser	Ser	Pro
				125					130				135	
Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	Gly	Ala	Leu	His	Arg	His
				140				145					150	
Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	Asp	Cys	Gly	Thr	Cys
				155				160					165	
Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro
				170				175					180	
Thr														

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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CTGCTGGGGG CCCGGGCCAG NGGCGGCACT CGTAGCCCCA GGTGTGACTG 50
TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTTC AGAGGGCTGCC 100
CAGCGGGGCA ACTACCTGAA GGCCCCTTGC ACGGAGCCCT GCGCAACTCC 150
ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCAACCA 200
TAATTCTGAA TGTGCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250
TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300
CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTCA 350

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CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400

ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1438 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGC GCGGAGGCCG AGAGAGAAAGT CACTGCCCT GGCTCTACCT 50

TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100

AGCTCTATCC TGTGCCCTG GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150

TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200

CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCCGCTCC 250

CCCCGCCCGC CAGGCGGGCC CTTCTCGACG GCGCGGGCGG GGCCCTGCGG 300

GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350

AGCCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCAGGGCTGC 400

CGGGCGGTGG CGGCGGCGCT CCTCCTGGTG CTGCTGGGG CCCGGGCCA 450

GGGCGGGACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500

AGATTGGTCT GTTTGTTGC AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550

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GCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600  
AGACACCTTC TTGGCCTGGG AGAACACCAC TAATTCTGAA TGTGCCCGCT 650  
GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700  
GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750  
CCAGGTCAGC CAATGTGTCA GCAGTTCACCC CTTCTACTGC CAACCATGCC 800  
TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850  
GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900  
CTGCGTGTCC TGCCCCACGT AATTCTAGC TGTCGTGGGAG TGGAGGGAAG 950  
GGCGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000  
CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050  
GTGGGCCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100  
GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACTTCA GCCAGCATTC 1150  
CCCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTGTCA CTTACACAGA 1200  
GAGTCACATT GATATAGCTT TAAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250  
CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGCA ACAGAGCGAG 1300  
ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350  
AATCTATTAA ATAAATAAAT ACAAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400  
TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTG 1438

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 417 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu  
1 5 10 15  
Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser  
20 25 30  
Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu  
35 40 45  
Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro  
50 55 60  
Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln  
65 70 75  
Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala  
80 85 90

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Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu  
95 100 105  
Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly  
110 115 120  
Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Pro  
125 130 135  
Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His  
140 145 150  
Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys  
155 160 165  
Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro  
170 175 180  
Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys  
185 190 195  
Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu  
200 205 210  
Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr Arg  
215 220 225  
His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly  
230 235 240  
Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu  
245 250 255  
Asp Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys  
260 265 270  
Ile Cys Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr  
275 280 285  
Pro Glu Thr Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp  
290 295 300  
Asp Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr  
305 310 315  
Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met Met Leu Gln  
320 325 330  
Pro Gly Pro Gln Leu Tyr Asp Val Met Asp Ala Val Pro Ala Arg  
335 340 345  
Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg Glu Ala Glu  
350 355 360  
Ile Glu Ala Val Glu Val Glu Ile Gly Arg Phe Arg Asp Gln Gln  
365 370 375  
Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu  
380 385 390  
Gly Ala Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys  
395 400 405

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Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro  
410 415

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGCTCTGG TGGCCCTTGC AGAACGCC 27

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCGGCCGAG AAGTTGAGAA ATGTC 25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1634 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACACAGACG GGCAGAGAGC 50

ACGGAGCCGG GAAGCCCCTG GGCGCCCGTC GGAGGGCT ATG GAG 94  
Met Glu  
1

CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133  
Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu  
5 10 15

CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172  
Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr  
20 25

CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211  
Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys  
30 35 40

AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250  
Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly  
45 50

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CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC GGC AAC 289  
His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn  
55 60 65

TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC 328  
Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala  
70 75 80

TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG 367  
Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln  
85 90

GCC TGT GAT GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC 406  
Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu Asn  
95 100 105

TGT TCA GCA GTG GCC GAC ACC CGC TGT GGC TGT AAG CCA 445  
Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro  
110 115

GGC TGG TTT GTG GAG TGC CAG GTC AGC CAA TGT GTC AGC 484  
Gly Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser  
120 125 130

AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC GGG 523  
Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly  
135 140 145

GCC CTG CAC CGC CAC ACA CGG CTA CTC TGT TCC CGC AGA 562  
Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg  
150 155

GAT ACT GAC TGT GGG ACC TGC CTG CCT GGC TTC TAT GAA 601  
Asp Thr Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu  
160 165 170

CAT GGC GAT GGC TGC GTG TCC TGC CCC ACG AGC ACC CTG 640  
His Gly Asp Gly Cys Val Ser Cys Pro Thr Ser Thr Leu  
175 180

GGG AGC TGT CCA GAG CGC TGT GCC GCT GTC TGT GGC TGG 679  
Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys Gly Trp  
185 190 195

AGG CAG ATG TTC TGG GTC CAG GTG CTC CTG GCT GGC CTT 718  
Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu  
200 205 210

GTG GTC CCC CTC CTG CTT GGG GCC ACC CTG ACC TAC ACA 757  
Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr  
215 220

TAC CGC CAC TGC TGG CCT CAC AAG CCC CTG GTT ACT GCA 796  
Tyr Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala  
225 230 235

GAT GAA GCT GGG ATG GAG GCT CTG ACC CCA CCA CCG GCC 835  
Asp Glu Ala Gly Met Glu Ala Leu Thr Pro Pro Pro Ala  
240 245

ACC CAT CTG TCA CCC TTG GAC AGC GCC CAC ACC CTT CTA 874  
Thr His Leu Ser Pro Leu Asp Ser Ala His Thr Leu Leu  
250 255 260

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GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC GTC CAG 913  
Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr Val Gln  
265 270 275

TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC 952  
Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr  
280 285

CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC 991  
Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp  
290 295 300

CAG TTG CCC AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC 1030  
Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro  
305 310

ACA CTC TCG CCA GAG TCC CCA GCC GGC TCG CCA GCC ATG 1069  
Thr Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met  
315 320 325

ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC GTG ATG GAC 1108  
Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp  
330 335 340

GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG 1147  
Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr  
345 350

CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG 1186  
Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val  
355 360 365

GAG ATC GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC 1225  
Glu Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu  
370 375

AAG CGC TGG CGC CAG CAG CAG CCC GCG GGC CTC GGA GCC 1264  
Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala  
380 385 390

GTT TAC GCG GCC CTG GAG CGC ATG GGG CTG GAC GGC TGC 1303  
Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys  
395 400 405

GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG T 1340  
Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro  
410 415 417

GACACGGCGC CCACCTGCCA CCTAGGCGCT CTGGTGGCCC TTGCAGAAC 1390

CCTAAGTACG GTTACTTATG CGTAGACA TTTTATGTCA CTTATTAAGC 1440

CGCTGGCACG GCCCTGCGTA GCAGCACCAAG CGGGCCCCAC CCCTGCTCGC 1490

CCCTATCGCT CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG 1540

GTGAAGACAT TTCTCAACTT CTCGGCCGGA GTTTGGCTGA GATCGCGGT 1590

TTAAATCTGT GAAAGAAAAC AAAAAAAA AAAAAAAA AAAA 1634

(2) INFORMATION FOR SEQ ID NO:10:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Val	Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile
1				5				10						15
Cys	Cys	Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys
				20				25						30
Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly
				35				40						45
Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys
				50				55						60
Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys
				65				70						75
Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr
				80				85						90
Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser
				95				100						105
Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln
				110				115						120
Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn
				125				130						135
Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr
				140				145						150

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Lys Leu Cys Leu

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 163 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys  
1 5 10 15  
Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr  
20 25 30  
Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr  
35 40 45  
Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser  
50 55 60  
Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu  
65 70 75  
Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu  
80 85 90  
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys  
95 100 105  
Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp  
110 115 120  
Val Val Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr  
125 130 135  
Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val  
140 145 150  
Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala Val Cys Thr  
155 160

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 170 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr Cys Arg Asp Gln Glu Lys Glu Tyr Tyr Glu Pro Gln His Arg  
1 5 10 15  
Ile Cys Cys Ser Arg Cys Pro Pro Gly Thr Tyr Val Ser Ala Lys  
20 25 30  
Cys Ser Arg Ile Arg Asp Thr Val Cys Ala Thr Cys Ala Glu Asn  
35 40 45

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Ser	Tyr	Asn	Glu	His	Trp	Asn	Tyr	Leu	Thr	Ile	Cys	Gln	Leu	Cys
50								55					60	
Arg	Pro	Cys	Asp	Pro	Val	Met	Gly	Leu	Glu	Glu	Ile	Ala	Pro	Cys
	65							70					75	
Thr	Ser	Lys	Arg	Lys	Thr	Gln	Cys	Arg	Cys	Gln	Pro	Gly	Met	Phe
	80							85					90	
Cys	Ala	Ala	Trp	Ala	Leu	Glu	Cys	Thr	His	Cys	Glu	Leu	Leu	Ser
	95							100					105	
Asp	Cys	Pro	Pro	Gly	Thr	Glu	Ala	Glu	Leu	Lys	Asp	Glu	Val	Gly
	110							115					120	
Lys	Gly	Asn	Asn	His	Cys	Val	Pro	Cys	Lys	Ala	Gly	His	Phe	Gln
	125							130					135	
Asn	Thr	Ser	Ser	Pro	Ser	Ala	Arg	Cys	Gln	Pro	His	Thr	Arg	Cys
	140							145					150	
Glu	Asn	Gln	Gly	Leu	Val	Glu	Ala	Ala	Pro	Gly	Thr	Ala	Gln	Ser
	155							160					165	
Asp	Thr	Thr	Cys	Lys										
	170													

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn	Leu	Glu	Gly	Leu	His	His	Asp	Gly	Gln	Phe	Cys	His	Lys	Pro
1				5					10					15
Cys	Pro	Pro	Gly	Glu	Arg	Lys	Ala	Arg	Asp	Cys	Thr	Val	Asn	Gly
				20				25						30
Asp	Glu	Pro	Asp	Cys	Val	Pro	Cys	Gln	Glu	Gly	Lys	Glu	Tyr	Thr
				35				40					45	
Asp	Lys	Ala	His	Phe	Ser	Ser	Lys	Cys	Arg	Arg	Cys	Arg	Leu	Cys
				50				55					60	
Asp	Glu	Gly	His	Gly	Leu	Glu	Val	Glu	Ile	Asn	Cys	Thr	Arg	Thr
				65				70					75	
Gln	Asn	Thr	Lys	Cys	Arg	Cys	Lys	Pro	Asn	Phe	Phe	Cys	Asn	Ser
				80				85					90	
Thr	Val	Cys	Glu	His	Cys	Asp	Pro	Cys	Thr	Lys	Cys	Glu	His	Gly
				95				100					105	
Ile	Ile	Lys	Glu	Cys	Thr	Leu	Thr	Ser	Asn	Thr	Lys	Cys	Lys	
				110				115						

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

- (A) LENGTH: 159 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala	Cys	Pro	Thr	Gly	Leu	Tyr	Thr	His	Ser	Gly	Glu	Cys	Cys	Lys
1									10					15
Ala	Cys	Asn	Leu	Gly	Glu	Gly	Val	Ala	Gln	Pro	Cys	Gly	Ala	Asn
				20					25					30
Gln	Thr	Val	Cys	Glu	Pro	Cys	Leu	Asp	Ser	Val	Thr	Phe	Ser	Asp
				35					40					45
Val	Val	Ser	Ala	Thr	Glu	Pro	Cys	Lys	Pro	Cys	Thr	Glu	Cys	Val
				50					55					60
Gly	Leu	Gln	Ser	Met	Ser	Ala	Pro	Cys	Val	Glu	Ala	Asp	Asp	Ala
				65					70					75
Val	Cys	Arg	Cys	Ala	Tyr	Gly	Tyr	Tyr	Gln	Asp	Glu	Thr	Thr	Gly
				80					85					90
Arg	Cys	Glu	Ala	Cys	Arg	Val	Cys	Glu	Ala	Gly	Ser	Gly	Leu	Val
				95					100					105
Phe	Ser	Cys	Gln	Asp	Lys	Gln	Asn	Thr	Val	Cys	Glu	Glu	Cys	Pro
				110					115					120
Asp	Gly	Thr	Tyr	Ser	Asp	Glu	Ala	Asn	His	Val	Asp	Pro	Cys	Leu
				125					130					135
Pro	Cys	Thr	Val	Cys	Glu	Asp	Thr	Glu	Arg	Gln	Leu	Arg	Glu	Cys
				140					145					150
Thr	Arg	Trp	Ala	Asp	Ala	Glu	Cys	Glu						
				155										

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala	Cys	Arg	Glu	Lys	Gln	Tyr	Leu	Ile	Asn	Ser	Gln	Cys	Cys	Ser
1				5					10					15
Leu	Cys	Gln	Pro	Gly	Gln	Lys	Leu	Val	Ser	Asp	Cys	Thr	Glu	Phe
				20					25					30
Thr	Glu	Thr	Glu	Cys	Leu	Pro	Cys	Gly	Glu	Ser	Glu	Phe	Leu	Asp
				35					40					45
Thr	Trp	Asn	Arg	Glu	Thr	His	Cys	His	Gln	His	Lys	Tyr	Cys	Asp
				50					55					60
Pro	Asn	Leu	Gly	Leu	Arg	Val	Gln	Gln	Lys	Gly	Thr	Ser	Glu	Thr
				65					70					75

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

Asp	Thr	Ile	Cys	Thr	Cys	Glu	Glu	Gly	Trp	His	Cys	Thr	Ser	Glu
80						85								90

  

Ala	Cys	Glu	Ser	Cys	Val	Leu	His	Arg	Ser	Cys	Ser	Pro	Gly	Phe
95						100								105

  

Gly	Val	Lys	Gln	Ile	Ala	Thr	Gly	Val	Ser	Asp	Thr	Ile	Cys	Glu
110									115					120

  

Pro	Cys	Pro	Val	Gly	Phe	Phe	Ser	Asn	Val	Ser	Ser	Ala	Phe	Glu
125									130					135

  

Lys	Cys	His	Pro	Trp	Thr	Ser	Cys	Glu	Thr	Lys	Asp	Leu	Val	Val
140									145					150

  

Gln	Gln	Ala	Gly	Thr	Asn	Lys	Thr	Asp	Val	Val	Cys	Gly		
155									160					

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ser	Cys	Pro	Glu	Arg	His	Tyr	Trp	Ala	Gln	Gly	Lys	Leu	Cys	Cys
1				5					10					15

  

Gln	Met	Cys	Glu	Pro	Gly	Thr	Phe	Leu	Val	Lys	Asp	Cys	Asp	Gln
									25					30

  

His	Arg	Lys	Ala	Ala	Gln	Cys	Asp	Pro	Cys	Ile	Pro	Gly	Val	Ser
									40					45

  

Phe	Ser	Pro	Asp	His	His	Thr	Arg	Pro	His	Cys	Glu	Ser	Cys	Arg
					50				55					60

  

His	Cys	Asn	Ser	Gly	Leu	Leu	Val	Arg	Asn	Cys	Thr	Ile	Thr	Ala
									65					75

  

Asn	Ala	Glu	Cys	Ala	Cys	Arg	Asn	Gly	Trp	Gln	Cys	Arg	Asp	Lys
									80					90

  

Glu	Cys	Thr	Glu	Cys	Asp	Pro	Leu	Pro	Asn	Pro	Ser	Leu	Thr	Ala
									95					105

  

Arg	Ser	Ser	Gln	Ala	Leu	Ser	Pro	His	Pro	Gln	Pro	Thr	His	Leu
									110					120

Pro

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

Thr	Cys	His	Gly	Asn	Pro	Ser	His	Tyr	Tyr	Asp	Lys	Ala	Val	Arg
1			5					10					15	
Arg	Cys	Cys	Tyr	Arg	Cys	Pro	Met	Gly	Leu	Phe	Pro	Thr	Gln	Gln
			20					25					30	
Cys	Pro	Gln	Arg	Pro	Thr	Asp	Cys	Arg	Lys	Gln	Cys	Glu	Pro	Asp
			35					40					45	
Tyr	Tyr	Leu	Asp	Glu	Ala	Asp	Arg	Cys	Thr	Ala	Cys	Val	Thr	Cys
			50					55					60	
Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	Pro	Cys	Ala	Trp	Asn	Ser
			65					70					75	
Ser	Arg	Val	Cys	Glu	Cys	Arg	Pro	Gly	Met	Phe	Cys	Ser	Thr	Ser
			80					85					90	
Ala	Val	Asn	Ser	Cys	Ala	Arg	Cys	Phe	Phe	His	Ser	Val	Cys	Pro
			95					100					105	
Ala	Gly	Met	Ile	Val	Lys	Phe	Pro	Gly	Thr	Ala	Gln	Lys	Asn	Thr
			110					115					120	
val	cys	glu												

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

His	Cys	Val	Gly	Asp	Thr	Tyr	Pro	Ser	Asn	Asp	Arg	Cys	Cys	His
1		5						10					15	
Glu	Cys	Arg	Pro	Gly	Asn	Gly	Met	Val	Ser	Arg	Cys	Ser	Arg	Ser
							20		25				30	
Gln	Asn	Thr	Val	Cys	Arg	Pro	Cys	Gly	Pro	Gly	Phe	Tyr	Asn	Asp
								35		40			45	
Val	Val	Ser	Ser	Lys	Pro	Cys	Lys	Pro	Cys	Thr	Trp	Cys	Asn	Leu
				50				55					60	
Arg	Ser	Gly	Ser	Glu	Arg	Lys	Gln	Leu	Cys	Thr	Ala	Thr	Gln	Asp
				65				70					75	
Thr	Val	Cys	Arg	Cys	Arg	Ala	Gly	Thr	Gln	Pro	Leu	Asp	Ser	Tyr
				80				85					90	
Lys	Pro	Gly	Val	Asp	Cys	Ala	Pro	Cys	Pro	Pro	Gly	His	Phe	Ser
				95					100				105	
Pro	Gly	Asp	Asn	Gln	Ala	Cys	Lys	Pro	Trp	Thr	Asn	Cys	Thr	Leu
				110					115				120	
Ala	Gly	Lys	His	Thr	Leu	Gln	Pro	Ala	Ser	Asn	Ser	Ser	Asp	Ala
				125					130				135	

Ile Cys Glu

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu  
1 5 10 15

Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu  
20 25 30

Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro  
35 40 45

Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr  
50 55 60

Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro  
65 70 75

Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr  
80 85 90

Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys  
95 100 105

Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp  
110 115 120

Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr  
125 130 135

Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu  
140 145 150

Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val  
155 160 165

Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val  
170 175 180

Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys  
185 190 195

Leu Pro

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

Met	Leu	Gly	Ile	Trp	Thr	Leu	Leu	Pro	Leu	Val	Leu	Thr	Ser	Val
1									10					15
Ala	Arg	Leu	Ser	Ser	Lys	Ser	Val	Asn	Ala	Gln	Val	Thr	Asp	Ile
					20				25					30
Asn	Ser	Lys	Gly	Leu	Glu	Leu	Arg	Lys	Thr	Val	Thr	Val	Glu	
					35				40					45
Thr	Gln	Asn	Leu	Glu	Gly	Leu	His	His	Asp	Gly	Gln	Phe	Cys	His
					50				55					60
Lys	Pro	Cys	Pro	Pro	Gly	Glu	Arg	Lys	Ala	Arg	Asp	Cys	Thr	Val
					65				70					75
Asn	Gly	Asp	Glu	Pro	Asp	Cys	Val	Pro	Cys	Gln	Glu	Gly	Lys	Glu
					80				85					90
Tyr	Thr	Asp	Lys	Ala	His	Phe	Ser	Ser	Lys	Cys	Arg	Arg	Cys	Arg
					95				100					105
Leu	Cys	Asp	Glu	Gly	His	Gly	Leu	Glu	Val	Glu	Ile	Asn	Cys	Thr
					110				115					120
Arg	Thr	Gln	Asn	Thr	Lys	Cys	Arg	Cys	Lys	Pro	Asn	Phe	Phe	Cys
					125				130					135
Asn	Ser	Thr	Val	Cys	Glu	His	Cys	Asp	Pro	Cys	Thr	Lys	Cys	Glu
				140				145						150
His	Gly	Ile	Ile	Lys	Glu	Cys	Thr	Leu	Thr	Ser	Asn	Thr	Lys	Cys
				155				160						165
Lys	Glu													

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 78 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Val	Val	Glu	Asn	Val	Pro	Pro	Leu	Arg	Trp	Lys	Glu	Phe	Val	Arg
1				5					10					15
Arg	Leu	Gly	Leu	Ser	Asp	His	Glu	Ile	Asp	Arg	Leu	Glu	Leu	Gln
					20				25					30
Asn	Gly	Arg	Cys	Leu	Arg	Glu	Ala	Gln	Tyr	Ser	Met	Leu	Ala	Thr
					35				40					45
Trp	Arg	Arg	Arg	Thr	Pro	Arg	Arg	Glu	Ala	Thr	Leu	Glu	Leu	Leu
					50				55					60
Gly	Arg	Val	Leu	Arg	Asp	Met	Asp	Leu	Leu	Gly	Cys	Leu	Glu	Asp
					65				70					75
Ile	Glu	Glu												

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile	Ala	Gly	Val	Met	Thr	Leu	Ser	Gln	Val	Lys	Gly	Phe	Val	Arg
1														15
Lys	Asn	Gly	Val	Asn	Glu	Ala	Lys	Ile	Asp	Glu	Ile	Lys	Asn	Asp
														30
Asn	Val	Gln	Asp	Thr	Ala	Glu	Gln	Lys	Val	Gln	Leu	Leu	Arg	Asn
														45
Trp	His	Gln	Leu	His	Gly	Lys	Lys	Glu	Ala	Tyr	Asp	Thr	Leu	Ile
														60
Lys	Asp	Leu	Lys	Lys	Ala	Asn	Leu	Cys	Thr	Leu	Ala	Glu	Lys	Ile
														75
														Gln Thr

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile	Cys	Asp	Asn	Val	Gly	Lys	Asp	Trp	Arg	Arg	Leu	Ala	Arg	Gln
1														15
Leu	Lys	Val	Ser	Asp	Thr	Lys	Ile	Asp	Ser	Ile	Glu	Asp	Arg	Tyr
														30
Pro	Arg	Asn	Leu	Thr	Glu	Arg	Val	Arg	Glu	Ser	Leu	Arg	Ile	Trp
														45
Lys	Asn	Thr	Glu	Lys	Glu	Asn	Ala	Thr	Val	Ala	His	Leu	Val	Gly
														60
Ala	Leu	Arg	Ser	Cys	Gln	Met	Asn	Leu	Val	Ala	Asp	Leu	Val	
														65
														70

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Asn	Arg	Pro	Leu	Ser	Leu	Lys	Asp	Gln	Gln	Thr	Phe	Ala	Arg	Ser
1														15

P1007P1D1seq1 (new)-response to 6-29-04 action.txt  
Val Gly Leu Lys Trp Arg Lys Val Gly Arg Ser Leu Gln Arg Gly  
20 25 30  
Cys Arg Ala Leu Arg Asp Pro Ala Leu Asp Ser Leu Ala Tyr Glu  
35 40 45  
Tyr Glu Arg Glu Gly Leu Tyr Glu Gln Ala Phe Gln Leu Leu Arg  
50 55 60  
Arg Phe Val Gln Ala Glu Gly Arg Arg Ala Thr Leu Gln Arg Leu  
65 70 75  
  
Val Glu

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ile Arg Glu Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys  
1 5 10 15  
Leu Gly Phe Thr Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr  
20 25 30  
Glu Arg Asp Gly Leu Lys Glu Lys Val Tyr Gln Met Leu Gln Lys  
35 40 45  
Trp Val Met Arg Glu Gly Ile Lys Gly Ala Thr Val Gly Lys Leu  
50 55 60  
Ala Gln Ala Leu His Gln Cys Ser Arg Ile Asp Leu Leu Ser Ser  
65 70 75  
  
Leu Thr

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ala Val Ala Phe Tyr Ile Pro Asp Gln Ala Thr Leu Leu Arg  
1 5 10 15  
Glu Ala Glu Gln Lys Glu Gln Gln Ile Leu Arg Leu Arg Glu Ser  
20 25 30  
Gln Trp Arg Phe Leu Ala Thr Val Val Leu Glu Thr Leu Lys Gln  
35 40 45  
Tyr Thr Ser Cys His Pro Lys Thr Gly Arg Lys Ser Gly Lys Tyr  
50 55 60

Arg Lys Pro

P1007P1D1seq1 (new)-response to 6-29-04 action.txt